

kinship matrix (K) was calculated using SPAGeDi-1.3c. Analysis of *Ppo-A1* and *Ppo-D1* variability showed 76.28% of cultivars carrying the *Ppo-A1a* allele and the remaining 23.71% with *Ppo-A1b*. In the case of *Ppo-D1*, 31.95% of the cultivars showed the *Ppo-D1a* allele and 68.05% presented *Ppo-D1b*. This is the first characterization of the genetic variability of *Ppo* genes in Argentinean hexaploid wheat germplasm. The association analysis showed that variation at the *Ppo-A1* locus was significantly related with PPO activity ($P = 0.0011$), with *Ppo-A1b* allele producing lower PPO activity (9.72 U) than *Ppo-A1a* (13.76 U). The *Ppo-D1* locus did not show significant association with the PPO activity in this AM panel ($P = 0.0943$). These results positioned *Ppo-A1b* allele as a valuable genetic tool to reduce PPO activity in the Argentinean bread wheat breeding programs.

Poster 37. Characterization of the effect of single and double *GPC-A1* and *GPC-D1* mutations in hexaploid wheat.

Assaf Distelfeld¹, Raz Avni¹, Stephen Pearce², Yan Jun³, Cristobal Uauy², Tzion Fahima³, and Jorge Dubcovsky².

¹ Faculty of Life Sciences, Department of Molecular Biology and Ecology of Plants, Tel Aviv University, Israel; ² Department of Plant Sciences, University of California, Davis, CA 95616, USA; and ³ Department of Evolutionary and Environmental Biology, University of Haifa, Mt. Carmel, Haifa 31905, Israel.

Plant senescence is a tightly regulated process designated to minimize the loss of minerals by maximizing remobilization to developing organs (e.g., seeds). The individual mechanisms and regulatory networks that define senescence are still poorly understood. In wheat, most of the nitrogen accumulated in the grain was already present in the plant at anthesis and is remobilized to the grains during maturation. Therefore, attempts to understand nutrient remobilization must consider senescence as an integral part of this complex process. Recently, the existence of a close connection between these two processes was shown through the map-based cloning of a wheat *GPC* (*Grain Protein Content 1*) gene. The *GPC-B1* gene encodes a NAC transcription factor associated with earlier senescence and increased grain protein, iron and zinc content in wheat. Recombinant inbred lines (RILs) of durum wheat carrying the functional allele from wild emmer wheat senesced 4–5 days earlier and had 5–10% higher grain protein, iron and zinc concentrations. In the current research, we have identified 'loss of function' ethyl methane sulphonate (EMS) mutants for the two homeologous genes, *GPC-A1* and *GPC-D1*, in hexaploid wheat. The mutants and control lines were grown under field conditions at four locations in Israel and characterized for their senescence patterns, *GPC*, and yield components. Our results showed a delay of senescence in both *gpc-A1* and *gpc-D1* mutants and a greater effect in the double mutant, *gpc-A1/gpc-D1*. Complete senescence of the single *gpc-A1* and *gpc-D1* mutants was delayed 10–20 days relative to the wild type control, and the difference increased to almost 70 days in the *gpc-A1/gpc-D1* double mutants. Grain protein content measurements in all mutants were lower than in wildtype plants, whereas grain yield was the same for all the tested genotypes suggesting the existence of different gene regulation for the accumulation of carbohydrates and minerals in the grain.

Poster 38. Development of *Thinopyrum distichum*-based, hexaploid tritipyrums.

Francois Marais. Department of Plant Sciences, North Dakota State University, Fargo, ND 58108, USA.

Thinopyrum distichum (Thunb.) Löve ($2n = 28 = J_1^d J_1^d J_2^d J_2^d$) is a highly salt-tolerant, perennial grass that is indigenous to the shoreline of Southern Africa where it grows within the spring high-tide zone. It is rhizomatous, exhibits facultative apomixis, and occupies highly saline coastal sands with low fertility, limited soil water, and high pH. Due to its adaptation to adverse environmental conditions, the grass has previously been targeted for gene mining and transfer to durum and common wheat, rye and triticale. It is furthermore a segmental autotetraploid and, in partial polyhaploids ($-J_1^d J_2^d$), its two genomes show a high degree of meiotic pairing. Two lineages of plants with $2n=42$ chromosomes that are presumed to have the genomic composition AABBJJ, were selected from segregating generations of crosses among primary and secondary *Triticum turdidum* subsp. *durum* / *Th. distichum* amphiploids. The J genome in each lineage is assumed to consist of seven *Thinopyrum* chromosomes. Because the plants are well developed, highly fertile, and produce well-developed seeds, their J genomes probably comprise full sets of homoeologous chromosomes, with each individual chromosome having been derived from either of the J_1^d or J_2^d genomes and altered through recombination with its homoeologue. In seedling salt-tolerance tests, the hybrids had high levels of salt tolerance comparable to those of the *Th. bessarabicum*-based tritipyrums that were developed at the John Innes Centre. One of the selections is free-threshing and without the brittle rachis trait.